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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:14:16 ; Search time 155 Seconds
(without alignments)
733.659 Million cell updates/sec

Title: US-09-787-126-2
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost		
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec		
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec		
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec		
5	1685	100.0	317	3	AAy84417	Aay84417 Amino aci		
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec		
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful		
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN		
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN		

10	1685	100.0	317	5	ABG31631	Abg31631	Human	RAN
11	1685	100.0	317	5	AAU78285	Aau78285	Human	TRA
12	1685	100.0	317	5	AAO19096	Aao19096	C neoform	
13	1685	100.0	317	6	ABP55108	Abp55108	Human	ost
14	1685	100.0	317	6	AAE34364	Aae34364	Human	rec
15	1685	100.0	317	6	ABR42314	Abr42314	Human	RAN
16	1685	100.0	317	7	ADB16988	Adb16988	Human	rec
17	1685	100.0	317	7	ADC35204	Adc35204	Human	TNF
18	1685	100.0	317	7	ADC73002	Adc73002	Human	RAN
19	1685	100.0	317	7	ADC78268	Adc78268	Human	RAN
20	1685	100.0	317	7	ABW02277	Abw02277	Human	RAN
21	1685	100.0	317	7	ADG46723	Adg46723	Human	RAN
22	1685	100.0	317	7	ADJ82112	Adj82112	Protein	f
23	1685	100.0	317	8	ADM96241	Adm96241	Human	rec
24	1677	99.5	317	2	AAW83018	Aaw83018	Osteoclas	
25	1422	84.4	270	7	ADJ82113	Adj82113	Protein	f
26	1417.5	84.1	316	2	AAW83017	Aaw83017	Osteoclas	
27	1417.5	84.1	316	2	AAW83194	Aaw83194	Human	ost
28	1417.5	84.1	316	2	AAW59654	Aaw59654	Amino	aci
29	1417.5	84.1	316	2	AAy17874	Aay17874	Murine	TR
30	1417.5	84.1	316	3	AAy91024	Aay91024	Mouse	OBM
31	1417.5	84.1	316	3	AAy84418	Aay84418	Amino	aci
32	1417.5	84.1	316	3	AAy84419	Aay84419	Amino	aci
33	1417.5	84.1	316	5	AAU78289	Aau78289	Mouse	TRA
34	1417.5	84.1	316	6	ABR42071	Abr42071	Human	RAN
35	1417.5	84.1	316	6	ABB99477	Abb99477	Amino	aci
36	1417.5	84.1	316	6	ABU08463	Abu08463	Amino	aci
37	1417.5	84.1	316	6	ABR55560	Abr55560	Amino	aci
38	1396.5	82.9	318	4	AAB82092	Aab82092	Rat	osteo
39	1326.5	78.7	294	2	AAW69956	Aaw69956	NF-kB	rec
40	1326.5	78.7	294	2	AAW68292	Aaw68292	NF-kB	rec
41	1326.5	78.7	294	2	AAE08737	Aae08737	Murine	re
42	1326.5	78.7	294	4	AAE04425	Aae04425	Murine	re
43	1326.5	78.7	294	4	AAE01992	Aae01992	Murine	RA
44	1326.5	78.7	294	5	AAE26102	Aae26102	Mouse	RAN
45	1326.5	78.7	294	7	ADB16986	Adb16986	Murine	re

ALIGNMENTS

RESULT 1

AAW83195

ID AAW83195 standard; protein; 317 AA.

XX

AC AAW83195;

XX

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.insert.

XX

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;

KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;

KW hypercalcaemia; osteoclast differentiation and activation receptor;

KW Paget's disease.

XX

OS Homo sapiens.

XX
 PN WO9846751-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-US007584.
 XX
 PR 16-APR-1997; 97US-00842842.
 PR 23-JUN-1997; 97US-00880855.
 PR 30-MAR-1998; 98US-00052521.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ;
 XX
 DR WPI; 1998-594578/50.
 DR N-PSDB; AAV70285.
 XX
 PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.
 PT treating bone diseases by modulating osteoclast differentiation and for
 PT diagnosis.
 XX
 PS Claim 19; Fig 4; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein. Host
 CC cells transfected with vectors containing nucleic acid molecules encoding
 CC OPG binding protein are used to produce recombinant OPG binding protein.
 CC OPG binding protein is used in binding assays to determine osteoprotegrin
 CC (OG) in biological samples; to screen for specific binding agents
 CC (particularly agonists and antagonists, including intracellular proteins)
 CC ; to raise Ab (useful in immunoassays for detection of OPG binding
 CC protein) and to identify compounds that modulate binding of OPG binding
 CC protein to osteoclast differentiation and activation receptor (ODAR). The
 CC nucleic acid molecule encoding OPG binding protein can be used to detect
 CC OPG binding protein-encoding sequences, e.g. screening for related
 CC sequences, also to produce transgenic animal models, while complementary
 CC sequences are used for antisense regulation of OPG binding protein
 CC expression. Modulators of OPG binding protein, particularly soluble forms
 CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,
 CC e.g. osteoporosis, bone loss caused by arthritis or metastases,
 CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
 CC loosening of prostheses, optionally in combination with agents that
 CC promote bone growth
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 |||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
 |||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

AAW69957

ID AAW69957 standard; protein; 317 AA.

XX

AC AAW69957;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF-kB receptor activator RANK ligand (RANKL).

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis; RANKL;

KW RANK ligand; tumour necrosis factor; TNF.

XX

OS Homo sapiens.

XX

PN WO9828426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US023775.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

DR WPI; 1998-377657/32.

DR N-PSDB; AAV41378.

XX

PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells.

XX

PS Claim 27; Page 59-60; 80pp; English.

XX

CC This represents a human RANKL, a ligand for the RANK (receptor activator
 CC of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
 CC tumour necrosis factor (TNF) family. A soluble RANK may be used for
 CC inhibiting activation of NF-kB, by contacting a cell expressing membrane-
 CC associated RANK with a soluble RANK which binds to RANK ligand (RANKL).
 CC RANKL polypeptides can activate RANK and can be used to induce maturation
 CC of dendritic cells and enhance their allo-stimulatory capacity, thereby
 CC augmenting an immune response. The soluble RANK polypeptide composition
 CC may also be used for regulating an immune or inflammatory response.
 CC Inhibition of NF-kB by RANK antagonists may be useful in ameliorating
 CC negative effects of an inflammatory response that result from triggering
 CC of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host
 CC reactions, or acute inflammatory reactions. They can also be used in
 CC adjunct therapy for disease characterised by neoplastic cells that
 CC express RANK. RANKL polypeptides can also be used to identify inhibitors
 CC of RANK and thus inhibitors of an inflammatory response, and also for
 CC protecting RANK-expressing cells from the negative effects of
 CC chemotherapy or the presence of high levels of TNF-alpha. The products
 CC can also be used for detection and drug screening
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 |||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
 |||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

 Qy 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 3
 AAW68293
 ID AAW68293 standard; protein; 317 AA.
 XX
 AC AAW68293;
 XX

DT 08-OCT-1998 (first entry)
 XX
 DE NF-kB receptor activator RANK ligand (RANKL).
 XX
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis; RANKL;
 KW RANK ligand; tumour necrosis factor; TNF.
 XX
 OS Homo sapiens.
 XX
 PN WO9828424-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US023866.
 XX
 PR 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 XX
 DR WPI; 1998-377655/32.
 DR N-PSDB; AAV41372.
 XX
 PT New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Example 7; Page 59-60; 80pp; English.
 XX
 CC This represents a human RANKL, a ligand for the RANK (receptor activator
 CC of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
 CC tumour necrosis factor (TNF) family. Host cells transformed or
 CC transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of NF-
 CC kB by RANK antagonists may be useful in ameliorating negative effects of
 CC an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
 |||

Database	Accession	Sequence	Length
Db	1	MRRASRDYTKYLGRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFNSGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFNSGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDODATYFGAFKVRDID	317

AAE08738

ID AAE08738 standard; protein; 317 AA.

XX

AC AAE08738;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX

KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;

KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN US6271349-B1.

XX

PD 07-AUG-2001.

XX

PF 17-DEC-1998; 98US-00215649.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 23-DEC-1996; 96US-00772330.

PR 07-MAR-1997; 97US-0077181P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

XX WPI; 1998-377655/32.
DR N-PSDB; AAD15311.
XX
PT New isolated receptor activator of necrosis factor-kappa B - useful for,
PT e.g. developing products for regulating an immune or inflammatory
PT response, treating toxic shock or sepsis.
XX
PS Example 15; Col 71-72; 47pp; English.
XX
CC The patent discloses novel receptor activator of nuclear factor (NF)-
CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of
CC the tumour necrosis factor (TNF) receptor superfamily and associates with
CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the
CC regulation of immune and inflammatory response. The receptors are useful
CC for regulating immune response and in screening for inhibitors of these
CC receptors. The cytoplasmic domain of RANK is used in developing assays
CC for inhibitors of signal transduction, e.g. for screening the molecules
CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and
CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful
CC in ameliorating the negative effects of an inflammatory response that
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
CC graft-versus-host reactions, acute inflammatory reactions and the effects
CC of bone resorption. RANK acts as an anti- apoptotic signal and rescue the
CC cells that express RANK from apoptosis. Soluble forms of the receptor are
CC used in vivo or in vitro based screening tests for agonists or
CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B
CC activation, or to inhibit transduction of a signal via RANK. RANK
CC compositions are used in the development of both agonistic and
CC antagonistic antibodies, or as an adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. Compounds that
CC interfere with RANK/TRAF6 interactions are useful for modulating the
CC formation of osteoclasts from osteoclast precursors and for modulating
CC osteoclast function and activities. They are used as inhibitors of
CC diseases associated with excess bone resorption and as immunosuppressants
CC or anti-inflammatory agents. The RANK DNAs are useful for the expression
CC of recombinant proteins, as probes for analysis of the presence or
CC distribution of RANK transcripts, while the proteins are useful in
CC preparing kits for the detection of soluble RANK, or monitor RANK-related
CC activity. The present sequence is RANK ligand (RANKL) protein from human
XX
SQ Sequence 317 AA;

[illegible]


```

Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
QY      181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db      181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
        |||
Db      301 PDQDATYFGAFKVRDID 317

```

RESULT 5

AA Y84417

ID AAY84417 standard; protein; 317 AA.

XX

AC AAY84417;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	49. .69
----	--------	---------

FT		/note= "transmembrane region"
----	--	-------------------------------

FT	Domain	70. .157
----	--------	----------

FT		/note= "extracellular stalk domain"
----	--	-------------------------------------

FT	Region	158. .317
----	--------	-----------

FT		/note= "active ligand moiety"
----	--	-------------------------------

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

DR N-PSDB; AAZ99964.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.

XX

PS Claim 19; Page 78-79; 110pp; English.

XX

CC The present sequence represents a human osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of OPGL
CC activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 3; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.2e-154;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

|||||

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

|||||

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

|||||

Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

|||||

Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

|||||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317

|||||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 6

AAE04426

ID AAE04426 standard; protein; 317 AA.

XX

AC AAE04426;

XX

DT 04-SEP-2001 (first entry)

XX
DE Human receptor activator of NF- χ B ligand (huRANKL) protein.
XX
KW Human; receptor activator of NF- χ B; RANK; tumour necrosis factor; TNF;
KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
KW chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 162. .317
FT /note= "Receptor binding region"
XX
PN US6242213-B1.
XX
PD 05-JUN-2001.
XX
PF 22-DEC-1997; 97US-00995659.
XX
PR 23-DEC-1996; 96US-0059978P.
PR 23-DEC-1996; 96US-00772330.
PR 07-MAR-1997; 97US-0077181P.
PR 14-OCT-1997; 97US-0064671P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM;
XX
DR WPI; 2001-407216/43.
DR N-PSDB; AAD08715.
XX
PT New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF- χ B
PT receptor activator) of the receptor activator of NF- χ B (RANK).
XX
PS Claim 1; Col 65-66; 43pp; English.
XX
CC The present invention relates to receptor activator of NF- χ B (RANK)
CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular
CC region. RANK associates with TNF receptor-associated factor (TRAF) 2 and
CC TRAF3. The DNA molecules are useful for producing ligands of RANK. The
CC ligands are useful for regulating immune response and in screening for
CC inhibitors of RANK. The present sequence is human RANKL (huRANKL) protein
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.2e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|||||
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 ||||||||||||||||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

AAE01993

ID AAE01993 standard; protein; 317 AA.

XX

AC AAE01993;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX

KW Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.

XX

OS Homo sapiens.

XX

PN WO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-US031459.

XX

PR 17-NOV-1999; 99US-00442029.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI; 2001-329222/34.

DR

N-PSDB; AAD05904.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Pagets disease and Familial Expansile Osteolysis (FEO).

XX

PS Disclosure; Page 76-77; 96pp; English.

XX

CC The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a Type I
CC transmembrane protein that interacts with TNF receptor-associated factors
CC (TRAFs). Triggering of RANK by overexpression or co-expression of RANK
CC and membrane bound RANK ligand (RANKL) results in upregulation of the
CC transcription factor NF-kappaB, a ubiquitous transcription factor that is
CC most extensively utilised in cells of the immune system. Inhibition of Nf
CC -kappaB by RANK antagonists is useful in ameliorating negative effects of
CC inflammatory reactions, and the effects of excess bone resorption. The
CC RANK DNAs, proteins and their analogues are useful for the preparation of
CC pharmaceutical compositions, for infecting target cells for use in gene
CC therapy applications in diagnosing diseases associated with RANK, and as
CC targets for use in screening assays. They may be used in the treatment or
CC diagnosis of immune system dysfunction. The present invention also
CC encompasses gene therapy methods to correct gene-activating mutations,
CC associated with e.g. familial expansile osteolysis (FEO) and early onset
CC Paget's disease of bone (EP). The present amino acid sequence is full-
CC length human RANKL (huRANKL) protein. The RANKL gene is located in
CC chromosome 13q14

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.2e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 PDQDATYFGAFKVRDID 317

ID ABB08134 standard; protein; 317 AA.
 XX
 AC ABB08134;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human RANKL polypeptide.
 XX
 KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
 KW tuberculostatic; cytostatic; human; RANKL.
 XX
 OS Homo sapiens.
 XX
 PN WO200236141-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 30-OCT-2001; 2001WO-US044834.
 XX
 PR 02-NOV-2000; 2000US-0245721P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
 PI Thomas EK;
 XX
 DR WPI; 2002-500114/53.
 XX
 PT Treating an individual suffering from infection, e.g. inflammation,
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilization factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells.
 XX
 PS Disclosure; Page 42-43; 43pp; English.
 XX
 CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human RANKL polypeptide fragment
 XX
 SQ Sequence 317 AA;

Query Match

100.0%; Score 1685; DB 5; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.2e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180
      |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 9

AAE26103

ID AAE26103 standard; protein; 317 AA.

XX

AC AAE26103;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human RANK ligand (RANKL) protein.

XX

KW Human; RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;

KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;

KW tumour necrosis factor receptor-associated factor; immunosuppressive;

KW antibacterial; antiinflammatory; chromosome 13.

XX

OS Homo sapiens.

XX

PN US2002086827-A1.

XX

PD 04-JUL-2002.

XX

PF 30-MAY-2001; 2001US-00871291.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-0077181P.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

PR 17-DEC-1999; 99US-00466496.

PR 24-MAY-2000; 2000US-00577800.

XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM;
XX
DR WPI; 2002-642254/69.
DR N-PSDB; AAD43213.
XX
PT A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))
PT polypeptide, useful for inhibiting activation of NF-kB and for regulating
PT an immune or inflammatory response in an individual.
XX
PS Example 15; Page 35; 49pp; English.
XX
CC The invention relates to novel RANK (receptor activator of nuclear factor
CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of
CC the invention are useful for inhibiting activation of NF-kappaB. They are
CC useful for regulating an immune or inflammatory response in an individual
CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB
CC by RANK antagonists is useful in ameliorating negative effects of an
CC inflammatory response that results from triggering of RANK, for e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions or acute
CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for
CC diseases characterised by neoplastic cells that express RANK. Soluble
CC forms of the receptor are useful in vitro to screen for agonists or
CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in
CC developing assays for inhibitors of signal transduction, to screen for
CC molecules that inhibit interaction of RANK with tumour necrosis factor
CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is
CC human RANK ligand (RANKL) protein. RANKL gene is located on chromosome 13
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.2e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300


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Qy      301 PDQDATYFGAFKVRDID 317
          |||
Db      301 PDODATYFGAFKVRDID 317
```

RESULT 10

ABG31631

ID ABG31631 standard; protein; 317 AA.

XX

AC ABG31631;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human RANKL protein.

XX

KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;

KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;

KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;

KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;

KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;

KW dendritic cell activator; T cell enhancer; human; RANKL.

XX

OS Homo sapiens.

XX

PN WO200266044-A2.

XX

PD 29-AUG-2002.

XX

PF 23-OCT-2001; 2001WO-US046254.

XX

PR 24-OCT-2000; 2000US-0242868P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;

XX

DR WPI; 2002-674891/72.

XX

PT Treating an individual with tumors or cancers, e.g. liver cancer or brain

PT tumor, by administering a combination of dendritic cell populations, T

PT cell enhancing factors and activated, antigen-specific T cells.

XX

PS Disclosure; Page 43-44; 44pp; English.

XX

CC The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human RANKL protein that was used in the method of the
CC invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

```

RESULT 11

AAU78285

ID AAU78285 standard; protein; 317 AA.

XX

AC AAU78285;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human TRANCE protein splice variant 1.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;

KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;

KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;

KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilagea;

KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;

KW cartilage growth; skeletal growth.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 126. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 137. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 140. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 145. .317

FT /note= "Specifically claimed in claims 17 and 18"


```

Db          |||||
61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPPFAHLTINATDIPSGSH 180
          |||||

Db          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPPFAHLTINATDIPSGSH 180

Qy          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||||

Db          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||||

Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
          |||||

Db          301 PDQDATYFGAFKVRDID 317

```

RESULT 12

AAO19096

ID AAO19096 standard; protein; 317 AA.

XX

AC AAO19096;

XX

DT 22-NOV-2002 (first entry)

XX

DE C neoformans antigen expressing dendritic cell related protein #5.

XX

KW Human; fungicide; fungal infection; dendritic cell; antigen;

KW Cryptococcus neoformans; vaccine; immunostimulant.

XX

OS Homo sapiens.

XX

PN WO200266053-A2.

XX

PD 29-AUG-2002.

XX

PF 14-DEC-2001; 2001WO-US048288.

XX

PR 04-JAN-2001; 2001US-0259653P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Thomas EK;

XX

DR WPI; 2002-674896/72.

XX

PT Producing a population of activated, Cryptococcus neoformans antigen-
PT presenting dendritic cells for preventing or treating C. neoformans
PT infection comprises causing the obtained dendritic cells to present the
PT antigen.

XX

PS Disclosure; Page 30-32; 32pp; English.

XX

CC The present invention relates to a method of producing a population of

XX
FH Key Location/Qualifiers
FT Domain 1. .47
FT /note= "putative cytoplasmic domain"
FT Domain 48. .68
FT /note= "putative transmembrane signal-anchor"
FT Domain 69. .317
FT /note= "putative extracellular domain"
FT Modified-site 171
FT /note= "potential N-glycosylation site"
FT Modified-site 198
FT /note= "potential N-glycosylation site"
XX
PN WO200276507-A2.
XX
PD 03-OCT-2002.
XX
PF 06-FEB-2002; 2002WO-US001238.
XX
PR 23-MAR-2001; 2001US-0278215P.
XX
PA (GETH) GENENTECH INC.
XX
PI Grewal I;
XX
DR WPI; 2003-058352/05.
DR N-PSDB; ABV75842.
XX
PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,
PT useful for treating immune related disorders such as autoimmune disease,
PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.
XX
PS Claim 1; Fig 1B; 111pp; English.
XX
CC The present sequence is the protein sequence of human osteoprotegerin
CC ligand (OPGL), a member of the tumour necrosis factor (TNF) family of
CC molecules that has been reported to bind to at least 2 receptors, RANK
CC and OPG. In the present invention, OPGL was shown to activate human
CC monocytes, and to activate such monocytes to secrete certain cytokines
CC such as interleukin-1 (IL-1), IL-6, IL-12, MIP-1alpha and TNF-alpha and
CC chemokines such as IL-8. OPGL may function in up-regulation of co-
CC stimulatory molecules such as ICAM-a and VCAM-1, LFA, and B7.1, B7.3 and
CC B7h. OPGL may also serve as an antigen presenting molecule which enhances
CC T-cell activation. The invention provides methods of using OPGL to
CC activate monocytes to secrete chemokines or cytokines by exposing a
CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided
CC are methods of using OPGL to treat conditions or diseases in mammals
CC associated with, or resulting from lack of, or decreased, chemokine or
CC cytokine secretion by monocytes. The invention also provides agonist and
CC antagonist molecules to modulate immune activity. These may include
CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti-
CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor
CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin
CC is used in a claimed method of treating an immune-related condition,
CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent
CC diabetes, osteoarthritis, inflammatory bowel disease (especially
CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 6.2e-154;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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RESULT 14

AAE34364

ID AAE34364 standard; protein; 317 AA.

XX

AC AAE34364;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human receptor activator of NF-kappa B ligand (RANKL).

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;

KW Cushing's syndrome; receptor activator of NF-kappa B ligand; cancer;

KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;

KW monocostotic fibrous dysplasia; radiation therapy; spinal cord injury;

KW RANKL; Gaucher's disease; polyostotic fibrous dysplasia; scurvy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .47

FT /note= "Intracellular domain"

FT Domain 48. .68

FT /note= "Transmembrane domain"

FT Domain 69. .317

FT /note= "Extracellular domain"
 FT Binding-site 162. .317
 FT /note= "RANK-binding domain"
 XX
 PN WO200292016-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 17-MAY-2002; 2002WO-US016002.
 XX
 PR 17-MAY-2001; 2001US-0291919P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Dougall WC, Anderson DM;
 XX
 DR WPI; 2003-129220/12.
 DR N-PSDB; AAD52598.
 XX
 PT Treating patients having e.g. acute septic arthritis, osteomalacia,
 PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises
 PT administering a receptor activator of NF-kappa B antagonist to increase
 PT bone formation.
 XX
 PS Claim 1; Page 51-52; 52pp; English.
 XX
 CC The invention relates to a method of treating a patient having e.g. acute
 CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome
 CC or spinal cord injury. The method involves administering a receptor
 CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the
 CC rate for formation of new bone. RANK antagonist is capable of inhibiting
 CC the ability of RANK to induce NF-kappa B. The method is useful for
 CC stimulating bone formation, or for treating patients having acute septic
 CC arthritis, osteomalacia (including rickets and scurvy),
 CC hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia,
 CC polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell
 CC histiocytosis, spinal cord injury, patients requiring periodontal
 CC reconstruction, or patients who have completed a course or radiation
 CC therapy for cancer. The method is also useful for treating a patient who
 CC is a prosthetic joint recipient, a bone graft recipient, or a ligament
 CC graft recipient. The invention is useful in gene therapy. The present
 CC sequence is human RANK ligand (RANKL) protein
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300
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Qy 301 PDQDATYFGAFKVRDID 317
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 Db 301 PDQDATYFGAFKVRDID 317

RESULT 15

ABR42314

ID ABR42314 standard; protein; 317 AA.

XX

AC ABR42314;

XX

DT 11-AUG-2003 (first entry)

XX

DE Human RANKL protein.

XX

KW Human; RANKL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic.

XX

OS Homo sapiens.

XX

PN WO2003040307-A2.

XX

PD 15-MAY-2003.

XX

PF 25-JUL-2002; 2002WO-US023782.

XX

PR 27-JUL-2001; 2001US-0307838P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Hilbert DH, Rosen CA;

XX

DR WPI; 2003-430659/40.

XX

PT New heteromultimeric complex having a first polypeptide member of the
 PT tumor necrosis factor (TNF) ligand family, and a second different member
 PT of TNF ligand family, useful for treating cancer, osteoporosis or an
 PT autoimmune disease.

XX

PS Disclosure; Page 366-367; 388pp; English.

XX

CC The present sequence is the protein sequence of human RANKL protein. The
 CC invention relates to compositions comprising heterotrimeric complexes of
 CC tumour necrosis factor (TNF) ligand family members, and their use in the
 CC detection, prevention and treatment of disease. In one embodiment, the

CC heterotrimeric complex comprises full-length or extracellular portions of
 CC RANKL and full-length or extracellular portions of other TNF ligand
 CC family members, preferably TRAIL. The heterotrimeric complexes of the
 CC invention are useful for treating an autoimmune disease, cancer or
 CC osteoporosis, and particularly for inhibiting cancer cell proliferation,
 CC increasing B cell proliferation, or inducing apoptosis of T cells. A
 CC claimed method of inhibiting cancer cell proliferation comprises
 CC administering a heterotrimeric complex consisting of TRAIL and CD40L or
 CC RANKL. A claimed method of treating osteoporosis comprises administering
 CC an antibody against a complex comprising RANKL and TRAIL
 XX
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAQVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAPHLTINATDIPSGSH	180
Db	121	QAFQGAQVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAPHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

Search completed: November 8, 2004, 18:28:12
 Job time : 159 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:26:09 ; Search time 40 Seconds
(without alignments)
525.570 Million cell updates/sec

Title: US-09-787-126-2
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result						Description
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			Query			
1	1685	100.0	317	3	US-08-996-139-13	Sequence 13, Appl
2	1685	100.0	317	3	US-08-995-659-13	Sequence 13, Appl
3	1685	100.0	317	3	US-09-215-649A-13	Sequence 13, Appl
4	1685	100.0	317	3	US-09-052-521C-4	Sequence 4, Appli
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, Appl
6	1685	100.0	317	4	US-09-577-800-13	Sequence 13, Appl
7	1685	100.0	317	4	US-09-466-496-13	Sequence 13, Appl
8	1685	100.0	317	4	US-09-871-856-13	Sequence 13, Appl
9	1685	100.0	317	4	US-09-871-291-13	Sequence 13, Appl
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17	1417.5	84.1	316	4	US-09-396-937-4	Sequence 4, Appli
18	1417.5	84.1	316	4	US-09-396-937-6	Sequence 6, Appli
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27	1326.5	78.7	294	4	US-09-877-650-11	Sequence 11, Appl
28	1326.5	78.7	294	4	US-09-865-363-11	Sequence 11, Appl
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32	721.5	42.8	188	4	US-09-396-937-14	Sequence 14, Appl
33	711.5	42.2	182	4	US-09-396-937-16	Sequence 16, Appl
34	691	41.0	173	4	US-09-396-937-18	Sequence 18, Appl
35	670	39.8	173	4	US-09-396-937-20	Sequence 20, Appl
36	418	24.8	77	4	US-09-632-287A-11	Sequence 11, Appl
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44	251.5	14.9	281	3	US-09-333-593A-6	Sequence 6, Appli
45	251.5	14.9	281	4	US-09-157-864-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-996-139-13

; Sequence 13, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-995-659-13

; Sequence 13, Application US/08995659

; Patent No. 6242213

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/995,659

; FILING DATE: 22 DECEMBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-995-659-13

Query Match 100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-215-649A-13

; Sequence 13, Application US/09215649A

; Patent No. 6271349

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,649A

; FILING DATE: 17-Dec-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

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; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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RESULT 4

US-09-052-521C-4

; Sequence 4, Application US/09052521C

; Patent No. 6316408

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors


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; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
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; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHTINATDIPSGSH 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHTINATDIPSGSH 180

Qy    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 5

US-09-577-780-13

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; Sequence 13, Application US/09577780
; Patent No. 6419929
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; GENERAL INFORMATION:

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; APPLICANT: Anderson, Dirk M.
;           Galibert, Laurent
;           Maraskovsky, Eugene
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```
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
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; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
```

```

;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/577,780
;      FILING DATE: 24-May-2000
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/995,659
;      FILING DATE: <Unknown>
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2852-A
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

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Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.7e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
      |||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
      |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

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Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 6

US-09-577-800-13

; Sequence 13, Application US/09577800

; Patent No. 6479635

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,800

; FILING DATE: 24-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/996,139

; FILING DATE: 22 DECEMBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-577-800-13

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
|
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180

Qy 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
|
Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
|
Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

US-09-466-496-13

; Sequence 13, Application US/09466496

; Patent No. 6528482

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/466,496

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; FILING DATE: 17-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-466-496-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
|
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240
|
Db    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
|
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 8


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Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
Db      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 9

US-09-871-291-13

; Sequence 13, Application US/09871291

; Patent No. 6562948

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 10

US-09-396-937-2

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; Sequence 2, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-396-937-2

Query Match 100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
| | | | |
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
| | | | |
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
| | | | |
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

QY 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
| | | | |
Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
| | | | |
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

QY 301 PDQDATYFGAFKVRDID 317
| | | | |
Db 301 PDQDATYFGAFKVRDID 317

RESULT 11

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. 6649164

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12
 US-09-865-363-13

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; Sequence 13, Application US/09865363
; Patent No. 6740522
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,363
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-865-363-13

```

```

Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF AHLTINATDIPSGSH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF AHLTINATDIPSGSH 180
 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
 Qy 301 PDQDATYFGAFKVRDID 317
 ||||||||||||||||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 13

US-08-842-842-7

; Sequence 7, Application US/08842842

; Patent No. 5843678

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91230-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/842,842

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-451

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-842-842-7

Query Match 84.1%; Score 1417.5; DB 2; Length 316;

Best Local Similarity 84.3%; Pred. No. 6.6e-136;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0686
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)852-9196
 ; TELEFAX: (650)496-1204
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 316 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-989-362-2

Query Match 84.1%; Score 1417.5; DB 3; Length 316;
 Best Local Similarity 84.3%; Pred. No. 6.6e-136;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
          ||||| ||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
          |||:| ||||| ||||| ||| ||||| ||:|:| |||:
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM 118

Qy    120 KQAFQGA VQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLTINATDIPSGS 179
          ||||| ||||| ||| ||:|:|:|:| ||| ||||| ||||
Db    119 KQAFQGA VQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
          |||:| ||||| ||||| ||||| ||||| ||||| |||:|:| |||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
          ||| ||||| ||||| ||||| ||||| |||||:|:|:|:| |||||
Db    239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKL RAGEEISIQVSNPSLL 298

Qy    300 DPDQDATYFGAFKVRDID 317
          ||||| |||||:|
Db    299 DPDQDATYFGAFKVQDID 316
  
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RESULT 15

US-09-052-521C-2

; Sequence 2, Application US/09052521C
 ; Patent No. 6316408
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 ; FILE REFERENCE: A-451Brv
 ; CURRENT APPLICATION NUMBER: US/09/052,521C
 ; CURRENT FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 08/880,855
 ; PRIOR FILING DATE: 1997-06-23
 ; PRIOR APPLICATION NUMBER: 08/842,842
 ; PRIOR FILING DATE: 1997-04-16
 ; NUMBER OF SEQ ID NOS: 40

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:15:11 ; Search time 39 Seconds
(without alignments)
782.070 Million cell updates/sec

Title: US-09-787-126-2
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	234	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis fac
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac

14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta -
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoprotocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A49733	[heparan sulfate]-
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU7L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

ALIGNMENTS

RESULT 1

I38707

Fas ligand - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: I38707; JC2340; S57565; I38554

R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A;Reference number: I38707; MUID:95127560; PMID:7826947

A;Accession: I38707

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-281 <RES>

A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.;

Fusamoto, H.; Kamada, T.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
 A;Reference number: JC2340; MUID:95071350; PMID:7980502
 A;Accession: JC2340
 A;Molecule type: DNA
 A;Residues: 1-281 <MIT>
 A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1;
 PID:g1369902
 R;Schatzlein, C.E.
 submitted to the EMBL Data Library, June 1995
 A;Reference number: S57565
 A;Accession: S57565
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-281 <SCH>
 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
 R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley,
 K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.
 J. Exp. Med. 181, 71-77, 1995
 A;Title: Fas ligand mediates activation-induced cell death in human T
 lymphocytes.
 A;Reference number: I38554; MUID:95105731; PMID:7528780
 A;Accession: I38554
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-281 <RE2>
 A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
 C;Genetics:
 A;Gene: FasL
 A;Introns: 151/1; 116/3
 C;Keywords: glycoprotein; transmembrane protein
 F;80-102/Domain: transmembrane #status predicted <TMM>
 F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;
 Best Local Similarity 21.7%; Pred. No. 2.2e-08;
 Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy	22	PGAPHEGPLHAPPPAP----	HQPPAASRS-----	MFVALLGLGLGQVVCS	63
				:	
Db	46	PPPPPPPLPPPPPPPLPPLPLPPLK	RGNHSTGLCLLMFFMVLVALVGLGLG	-----	100
Qy	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF			123
		:	: : :		
Db	101	--MFQLFHLQ-----	KELAELESTSQMHTA-----		124
Qy	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFALHT--INATDIPSGSHK			181
		: : :	:	: :	
Db	125	--SSLEKQIGH-----	PSPPPEKKELRKVAHLTGKNSRSMP-----		159
Qy	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMVY			241
		: : : : : :			
Db	160	---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----	LPLSHK		210
Qy	242	VTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEFHFYSINVGFFKLRSGEEISIEVSN		295
		: : :	: : : :		
Db	211	VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----	YLGAVFNLTSAHDLYVNVSE		263

QY 296 PSLLDPDQDATYFGAFKV 313
||:: :: |:|| ::
Db 264 LSLVNFEESQTFFGLYKL 281

RESULT 2

A53062

Fas ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.

Cell 76, 969-976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.

A;Reference number: A53062; MUID:94185175; PMID:7511063

A;Accession: A53062

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-279 <TAK>

A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAA17800.1;

PID:g473565

Query Match 10.9%; Score 184.5; DB 2; Length 279;
Best Local Similarity 21.7%; Pred. No. 5.3e-08;
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPLHAPPPAPHPQ-----PAASRSMFVALLGLGL 57
|| :: | | || | | | | : |||:|:|
Db 38 RGPDQRRPPPPPPVSPPLPPPSQPLPLPLPTPLKKKDHTNLWLPPVFFMVLVALVGMGL 97

Qy 58 GQVVC SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
| :|:: |
Db 98 G-----MYQLFHL----- 105

Qy 118 RIKQAFQGA VQKELQHI--VGSQHIRA---EKAMVDG SWLDLAKRSKLEAQPFAHLTINA 172
|||| : :| :: || : : | | : ||| |
Db 106 -----QKELAE LREFTNQSLKVSSF EKQIANPS----TPSEKKEPRSV AHLTGN- 150

Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
| : | | || : : | |::|: | |::|: : || :
Db 151 -----PHSR SIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201

Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISI 291
: | ||: : | | ||: | : : | : | | | : : :
Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV 257

Qy 292 EVSNPSLLDPDQDATYFGAFKV 313
:| ||:: :: |:|| ::
Db 258 NISQLSLINFEESKTFFGLYKL 279

RESULT 3

S53090

CD40 ligand - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1;
PID:g732570

Query Match 10.5%; Score 176.5; DB 2; Length 261;
Best Local Similarity 24.2%; Pred. No. 2.3e-07;
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

```
Qy      33 PPPPAPHQPPAASRSMFVALLGLGL-GQVVC SVALFFYFRAQMDPNRISEDGTHCIYRIL 91
      | | : | | : | : | | : | | : | | : | | : | | : |
Db      8 PSPRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R 57

Qy      92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG 149
      |||: | | : | : | : | : | : | : | : | : | : | : |
Db      58 NLHEDFVFMKTIQRCNKGE GSSLNCEEIRS RFEDLVKDIMQ----NKEVKKKEKNFE- 112

Qy     150 SWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSLS SWYHDRGWAKISN--MTFSNGK-L 206
      : | | ||: | : | | : | : | : | : | : | : | : |
Db     113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYTLSNNLVTLENGKQL 161

Qy     207 IVNQDGFYYLYANICFRH HETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
      | : ||||: | : | : | : | : | : | : | : | : | : |
Db     162 AVKRQGFYYIYTQVTFC SNR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212

Qy     265 SGNSEFH FYSINVG GFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
      | : ||: || | : | : | : | : | : | : | : | : |
Db     213 SSSKPCGQQSIHLGGVFELQSGASVFVNVTDP SQVSHGTGFTSFGLLKL 261
```

RESULT 4

A49266

fas ligand - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A49266

R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.

Cell 75, 1169-1178, 1993

A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.

A;Reference number: A49266; MUID:94084792; PMID:7505205

A;Accession: A49266

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-278 <SUD>

A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178; PIDN:AAC52129.1;

PID:g440179

C;Keywords: glycoprotein; transmembrane protein

Query Match 10.4%; Score 175.5; DB 2; Length 278;
 Best Local Similarity 20.3%; Pred. No. 3e-07;
 Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

```

Qy      21 GPGAPHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLGL 57
      ||| | |||:| ||: | |||:|:|
Db      39 GPGQRRPPP--PPPPSPLPSPSQFPPLPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96

Qy      58 GQVVCVALFFYFRAQMDPNRISEGDTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
      | : | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      97 G-----MYQLFHLQKELAEELREFTNHSL-RVSSFQKQIANPSTPSETKKPRSV----- 143

Qy     118 RIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPS 177
      ||| |
Db     144 -----AHLTG NPR----- 151

Qy     178 GSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
      | : | | | | | : : | | : : | | : : | | : : | : : |
Db     152 -SRSIPL-EWEDTYGTALISGVKYYKKGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205

Qy     238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPS 297
      ||: : | | ||: | : : | : | | | : : : | |
Db     206 HKVYM--RNFKYPGDLVLMEEKKLNCT-TGQIAHSSYLGAVFNLTVDHLYVNISQLS 262

Qy     298 LLDPDQDATYFGAFKV 313
      |: : | : | : |
Db     263 LINFEESKTFFGLYKL 278
  
```

RESULT 5

I53476

CD40 ligand - human

N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593

R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; Noelle, R.J.; Stamenkovic, I.; Ledbetter, J.A.; Aruffo, A. EMBO J. 11, 4313-4321, 1992

A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity.

A;Reference number: S28017; MUID:93049181; PMID:1385114

A;Accession: S28017

A;Molecule type: mRNA

A;Residues: 1-261 <HOL>

A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484

R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.A.; Maliszewski, C.R.; Fanslow, W.C. J. Exp. Med. 176, 1543-1550, 1992

A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.

A;Reference number: JH0793; MUID:93094757; PMID:1281209

A;Accession: JH0793

A;Molecule type: mRNA

A;Residues: 1-261 <SPR>
 A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
 A;Experimental source: peripheral blood T-cell
 R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; KroczeK, R.A.
 Eur. J. Immunol. 22, 3191-3194, 1992
 A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A;Reference number: S26694; MUID:93076854; PMID:1280226
 A;Accession: S26694
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-261 <GRA>
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.;
 Bonnefoy, J.Y.
 FEBS Lett. 315, 259-266, 1993
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and
 regulation of expression by factors controlling IgE production.
 A;Reference number: S28852; MUID:93138085; PMID:7678552
 A;Accession: S28852
 A;Molecule type: mRNA
 A;Residues: 1-261 <GAU>
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having
 6-Gln
 C;Genetics:
 A;Gene: GDB:CD40LG; HIGM1; IMD3
 A;Cross-references: GDB:120632; OMIM:308230
 A;Map position: Xq26-Xq26
 C;Keywords: glycoprotein; transmembrane protein
 F;13-44/Domain: transmembrane #status predicted <TMM>
 F;45-261/Domain: extracellular #status predicted <EXT>
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;
 Best Local Similarity 24.5%; Pred. No. 7.7e-06;
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

```

Qy      45 SRSMFVALLGLGL-GQVVCVALFFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT- 102
      |  ::  || : |  |:: |      |  ::|  :| ::      |||: | |
Db      20 SMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----RNLHEDFVFMKTI 69

Qy      103 -TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
      : : |  :|  ||  |:: |  ::      : | :  : | : : | :
Db      70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKKENSF-EMQKGDQ-N 119

Qy      162 AQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
      | ||:  |:  |  | : |  ::| :|  ||| | | : | ||: ||
Db      120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173

Qy      219 NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
      : | : : |  ::  :| |  |:: :| |  ||:
Db      174 QVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224

Qy      277 VGGFFKLRSGEESIEVSNPSLLDPDQDATYFGAFKV 313
      :|| |:: | : : |::|| :  | || | :
Db      225 LGGVFELQPGASVFVNVDPSQVSHGTGFTSFGLLKL 261
  
```

RESULT 6

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.

A;Reference number: A22908; MUID:88224564; PMID:2836146

A;Accession: A22908

A;Molecule type: DNA

A;Residues: 1-235 <SHI>

A;Cross-references: UNIPROT:P06804; GB:M20155

R;Shakhov, A.N.; Nedospasov, S.A.

Bioorg. Khim. 13, 701-705, 1987

A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.

A;Reference number: S03791; MUID:87298639; PMID:3040015

A;Accession: S03791

A;Molecule type: DNA

A;Residues: 1-235 <SHA>

A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A;Note: article in Russian with English abstract

R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha- (tumor necrosis factor) and TNF-beta- (lymphotoxin) genes.

A;Reference number: A93679; MUID:88067722; PMID:3684584

A;Accession: A27303

A;Molecule type: DNA

A;Residues: 1-235 <SEM>

A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.

A;Reference number: A25164; MUID:85298296; PMID:3898078

A;Accession: A25164

A;Molecule type: mRNA

A;Residues: 1-235 <PEN>

A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.;

Kawashima, E.; Chollet, A.; Tizard, R.; van Heuverswyn, H.; van Vliet, A.;

Ruysschaert, M.R.; Fiers, W.

Nucleic Acids Res. 13, 4417-4429, 1985

A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.

A;Reference number: A23127; MUID:85242112; PMID:2989794

A;Accession: A23127

A;Molecule type: mRNA

A;Residues: 1-235 <FRA>

A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R;Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein.
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A. Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of mRNA molecules specifying inflammatory mediators.
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A. Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor.
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;
Best Local Similarity 25.9%; Pred. No. 0.00018;
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSL-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |          |:| | | | :|| | : :|| || | :|: :
Db      90 KPAHVVAN-----HQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:      |      :|: | |::      :|| |      :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCKDTPGAELKPW---- 192

Qy      269 EFHFYSINVGFFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| ||: | || : |||
Db      193 ---YEPIYLGGVFQLEKGDQLSAEVLNLPKYLDFAESGQVYFG 231

```

RESULT 7
A25451
tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A25454; A25451; JS0727
 R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.
 DNA 5, 149-156, 1986
 A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor.
 A;Reference number: A25454; MUID:86219711; PMID:3519137
 A;Accession: A25454
 A;Molecule type: mRNA
 A;Residues: 1-234 <ITO>
 A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A;Reference number: A25451; MUID:86219712; PMID:3519138
 A;Accession: A25451
 A;Molecule type: DNA
 A;Residues: 1-234 <IT2>
 A;Note: this sequence differs from that shown in having a Gln inserted between residues 62 and 63
 R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).
 A;Reference number: JH0309; MUID:91065534; PMID:2249779
 A;Accession: JS0727
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-62,'Q',63-234 <SHA>
 A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C;Genetics:
 A;Introns: 62/3; 80/1; 96/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
 F;1-81/Domain: propeptide #status predicted <PRO>
 F;82-234/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;
 Best Local Similarity 21.6%; Pred. No. 0.0002;
 Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

```

Qy      27  EGPLHAPPPAPHQPPAASR----SMFVALLGLGLGQVVCVVALFFYFRAQMDPNRISED 82
      |||| | : | |:| || | : | :|
Db      14  EGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGATTLCF----LLHFRVIGPQEEESPN 65

Qy      83  GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRA 142
      | : | | || |

```

Db 66 NLHLV-----NPVAQMVTLS-----A 82
 Qy 143 EKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTF 201
 :|:| | :| ||: | | :| | | :| |
 Db 83 SRALSD-----KPLAHVVAN----PQVEGQL---QWLSQRANALLANGMKL 121
 Qy 202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258
 :: :|:| || | :|: : | || | :| | |:: :: |: |: |
 Db 122 TDNQLVVPADGLYLIYSQVLF-----SGQGCRSYVLLTHTVSRFAVSYPNKNVLLSAIKS 176
 Qy 259 -----GSTKYWSGNSEFHFYSINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYF 308
 | : | :|| |:| |:| :| ||: | || : ||
 Db 177 PCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYF 229
 Qy 309 G 309
 |
 Db 230 G 230

RESULT 8

JH0529

tumor necrosis factor alpha precursor - sheep

N;Alternate names: cachectin; TNF alpha

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JH0529; S48118; S13114; S20661

R;Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.

A;Reference number: JH0529; MUID:92112044; PMID:1765267

A;Accession: JH0529

A;Molecule type: mRNA

A;Residues: 1-234 <GRE>

A;Cross-references: UNIPROT:P23383; EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A;Experimental source: alveolar macrophage

R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A;Reference number: S48118; MUID:92155784; PMID:1786996

A;Accession: S48118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-234 <NAS>

A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A;Reference number: S13114; MUID:91067496; PMID:2251151

A;Accession: S13114

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-62,64-234 <YOU>

A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A;Note: comparison with the introns of homologous sequences suggest that this is probably an alternative splicing

A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-233 <IRI>
 A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.; Goeddel, D.V.
 Nature 312, 724-729, 1984
 A;Title: Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin.
 A;Reference number: A93351; MUID:85086244; PMID:6392892
 A;Accession: A93351
 A;Molecule type: mRNA
 A;Residues: 1-233 <PEN>
 A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukemia
 R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Yamamoto, R.; Mark, D.F.
 Science 228, 149-154, 1985
 A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A;Reference number: A44189; MUID:85142190; PMID:3856324
 A;Accession: A44189
 A;Molecule type: mRNA
 A;Residues: 1-62,'S',64-233 <WAN>
 A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
 R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.; Sugimoto, T.; Kurimoto, M.
 Lymphokine Res. 7, 175-185, 1988
 A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-alpha from BALL-1 cells stimulated by HVJ.
 A;Reference number: A61478; MUID:88301617; PMID:2841543
 A;Accession: B61478
 A;Molecule type: protein
 A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,'X',182-204 <FUK>
 R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.
 Eur. J. Biochem. 152, 515-522, 1985
 A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor nectosis factor.
 A;Reference number: I53311; MUID:86030296; PMID:3932069
 A;Accession: I53311
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <MAR>
 A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
 A;Experimental source: U-937 cells
 R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A;Reference number: S62610; MUID:96202967; PMID:8631363
 A;Accession: S62610
 A;Molecule type: protein

A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region.
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel, D.V.; Harkins, R.N.
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction, TNF-alpha can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others without detriment to normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;
Best Local Similarity 25.5%; Pred. No. 0.00094;
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
:| ||: | | : : | | :| : :||: :| :| :
Db 87 KPAHVVAN----PQAEQQL---QWLNRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139
Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273

```

      |:  :: || : : ||  ::|| |  :| . ||  :
Db      140 FKGQGPCSTHVLTLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      | :|| |:| |: :| |: : | || :   |||
Db      193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229

```

RESULT 10

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C;Species: Peromyscus leucopus (white-footed mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I54490

R;Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae).

A;Reference number: I54490; MUID:92218012; PMID:1348497

A;Accession: I54490

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-235 <RES>

A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C;Genetics:

A;Gene: PlTNF

A;Introns: 62/3; 81/1; 97/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

```

Query Match          7.9%;  Score 132.5;  DB 2;  Length 235;
Best Local Similarity 25.3%;  Pred. No. 0.0011;
Matches  42;  Conservative  27;  Mismatches  54;  Indels  43;  Gaps  7;

```

```

Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMFTFSNG-----KLIVNQDGFYYL 216
      :| ||: |      |:|      : ||      :||      :||: || | :
Db      90 KPAHVVAN-----HQVDEQLEWLSRG----ANALLANGMDLKDNLVIPADGLYLV 137

Qy      217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264
      |: : |:      | : |: |      |::      :|| |      :|  ||
Db      138 YSQVLFK-----GQGCSSYVLLTHTVSRFAVSIEDKVNLLSAIKSPCPKETPEGSELKPW 192

Qy      265 SGNSEFHFYSINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      : | :|| |:| |: :| ||: | || :   |||
Db      193 -----YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

```

RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
 Agric. Biol. Chem. 53, 1733-1736, 1989
 A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.
 A;Reference number: JU0029
 A;Accession: JU0029
 A;Molecule type: DNA
 A;Residues: 1-235 <SHI>
 A;Cross-references: UNIPROT:P16599
 R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
 Gene 132, 227-236, 1993
 A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
 A;Reference number: JN0868; MUID:94040766; PMID:8224868
 A;Accession: JN0868
 A;Molecule type: DNA
 A;Residues: 1-235 <KWO>
 A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
 R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
 Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
 A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.
 A;Reference number: S21674; MUID:92329007; PMID:1627266
 A;Accession: S21674
 A;Molecule type: mRNA
 A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
 A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
 C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and produces hemorrhagic necrosis of tumors.
 C;Genetics:
 A;Gene: TNF-alpha
 A;Introns: 62/3; 81/1; 97/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
 F;80-235/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;
 Best Local Similarity 25.3%; Pred. No. 0.0013;
 Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

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Qy      163 QPFAHLTINATDIPSGSHKVSL-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:          |  |  | :|| |  : :||| || | :|: :
Db      90 KPAHVAVN-----HQAEQLEWLSQRANALLANGMDLKDNLVVPADGLYLIYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:          |  :|: |  |::          :||| |  :|  | |
Db      142 LFK-----QGCPDYVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPW---- 192

Qy      269 EFHFYSINVGGFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309
          :  : :|| |:|  |:: |  ||: |  ||  :  |||
Db      193 ---YEPMYLGGVFQLEKGDLLSAEVLNPKYLDITESGQVYFG 231

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RESULT 12

I49139

lymphotoxin-beta - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49139; I49138; I49076

R;Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.

J. Immunol. 154, 239-246, 1995

A;Title: Characterization of the mouse lymphotoxin-beta gene.

A;Reference number: I49138; MUID:95088371; PMID:7995944

A;Accession: I49139

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-306 <RES>

A;Cross-references: UNIPROT:P41155; EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831

A;Accession: I49138

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-306 <RE3>

A;Cross-references: EMBL:U16984; NID:g577431; PIDN:AAB60493.1; PID:g577432

R;Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov,

S.V.; Novobrantseva, T.I.; Turetskaya, R.L.; Green, J.E.; Nedospasov, S.A.

Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995

A;Title: Cloning and expression analysis of the murine lymphotoxin beta gene.

A;Reference number: A55602; MUID:95148600; PMID:7846035

A;Accession: I49076

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-306 <RE2>

A;Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509

C;Genetics:

A;Gene: LT-beta

A;Introns: 54/3; 160/1

Query Match 7.7%; Score 130.5; DB 2; Length 306;

Best Local Similarity 22.1%; Pred. No. 0.0022;

Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

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Qy      105 ESQDTKLIP---DSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLE 161
          | : | : | | : : | : | | | | : : : | : :
Db      86 ETPDPR LHPQRSNASRNLASTSQGPV-----AQSSREASAWMTI----- 124

Qy      162 AQPFAHLTIN--ATDIPSGSHKVSLS-----SWYHDRG--WAKISNMTF----- 201
          | | | : : | | : | : : | : | | | | |
Db      125 LSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQ 184

Qy      202 ---SNGKLIVNQDGFYYLYANICFR--HHETSGDLATEYLQL--MVYVTKTSIKIPSSHTL 255
          : : | | : | | | | | : : | : | | : | : | |
Db      185 FSPTHG-LALPDQGVYYLYCHVG YRGRTPPAGRSRARS LTLRSALYRAGGAYGRGSPELL 243

Qy      256 MKGGST-----KYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQD 304
          : : | | : : | : | : | : | : | : | : | :
Db      244 LEGAETVTPVVDPIGYGSLW-----YTSVGFGGLAQLRSGERVYVNISHPDMVDYRRG 296

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Qy      305 ATYFGAFKV 313
          | : | | |
Db      297 KTEFGAVMV 305

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RESULT 13

S22052

tumor necrosis factor alpha precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C;Accession: S22052

R; Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A;Reference number: S22052

A:Accession: S22052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <SAN>

A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1;
PID:g38160

C;Genetics:

A; Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.7%; Score 130; DB 1; Length 233;

Best Local Similarity 25.5%; Pred. No. 0.0017;

Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSGKLIVNQDGFFYYLYANIC 221
 : | | : | : : | : | : : | : : : : | : | : : :

Db 87 KPVAVHVAN----POAEGOL---OWLNRRANALLANGVELRDNOLVVPSEGLYLIYSQVL 139

Qy 222 FRHH--ETSGDLATEYLQIMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
|: :: || : : || ::|| :| || :

Db 140 FKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy 274 SINVGGF~~FK~~LRSGEEISIEVSNPSLLD-PDQDATYFG 309

_____ | : || | : | | : : | : : | | | : | || |

Db 193 PIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229

RESULT 14

JO1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

C;Accession: J01344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 7.6%; Score 128; DB 1; Length 234;
Best Local Similarity 24.2%; Pred. No. 0.0025;
Matches 39; Conservative 32; Mismatches 58; Indels 32; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
:| ||: | | : : | | | :| : : :|:| || | :| : :
Db 88 KPVAHVVAN----PQAEQQL---QWLSGRANALLANGVKLTDNQLVVPLDGLYLIYSQVL 140
Qy 222 FRHHETSGDLATEYQLQLMVYVTKTSIKIPSSHTLMKG-----GSTKYWSGNSE 269
|: | :| | | : : : : || | : | :
Db 141 FK---GQGCPSTHVL-LTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPW----- 191
Qy 270 FHFYSINVGFFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
: | :|| | :| | : :| | : : | : | : || : |||
Db 192 --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230

RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor
 C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F;20/Binding site: myristate (Lys) (covalent) #status predicted
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 126.5; DB 1; Length 233;
 Best Local Similarity 25.5%; Pred. No. 0.0033;
 Matches 50; Conservative 25; Mismatches 80; Indels 41; Gaps 9;

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Qy      134 IVGSQHIRAEKAMVDGSLDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSWYHD 190
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Db      55 VIGPQREESPGGPSINSPLVQTLRSSSQASSNKPVAHV---VADINSPGQL----- 102

Qy      191 RGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDLATE 234
      | | :| :| | :| | | | :| :| | | :|
Db      103 RWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFQGGCPSTPLFLTHTISRIAVS 162

Qy      235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVS 294
      | | | : :| | | : | | : | | | :| :| :|
Db      163 Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYQGGVFQLEKGDRLSAEIN 213

Qy      295 NPSLLD-PDQDATYFG 309
      | | : | |
Db      214 LPDYLDYAESGQVYFG 229
  
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Search completed: November 8, 2004, 18:28:56
 Job time : 42 secs

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:29:02 ; Search time 170 Seconds
(without alignments)
658.662 Million cell updates/sec

Title: US-09-787-126-2
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1685	100.0	317	9	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	9	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	9	US-09-957-944-6	Sequence 6, Appli
4	1685	100.0	317	9	US-09-865-363-13	Sequence 13, Appl
5	1685	100.0	317	9	US-09-871-291-13	Sequence 13, Appl
6	1685	100.0	317	9	US-09-877-650-13	Sequence 13, Appl
7	1685	100.0	317	14	US-10-151-071-10	Sequence 10, Appl
8	1685	100.0	317	14	US-10-218-547-22	Sequence 22, Appl
9	1685	100.0	317	14	US-10-405-878-13	Sequence 13, Appl
10	1685	100.0	317	14	US-10-167-182-11	Sequence 11, Appl
11	1685	100.0	317	14	US-10-310-793-28	Sequence 28, Appl
12	1685	100.0	317	14	US-10-460-623-11	Sequence 11, Appl
13	1685	100.0	317	15	US-10-289-456-79	Sequence 79, Appl
14	1685	100.0	317	15	US-10-202-062-22	Sequence 22, Appl
15	1685	100.0	317	16	US-10-664-801-2	Sequence 2, Appli
16	1685	100.0	317	16	US-10-381-160-6	Sequence 6, Appli
17	1685	100.0	317	17	US-10-799-345-12	Sequence 12, Appl
18	1424.5	84.5	316	9	US-09-957-944-8	Sequence 8, Appli
19	1424.5	84.5	316	17	US-10-799-345-10	Sequence 10, Appl
20	1422	84.4	270	15	US-10-289-456-80	Sequence 80, Appl
21	1417.5	84.1	316	10	US-09-079-569-7	Sequence 7, Appli
22	1417.5	84.1	316	10	US-09-873-829-4	Sequence 4, Appli
23	1417.5	84.1	316	13	US-10-017-910-4	Sequence 4, Appli
24	1417.5	84.1	316	14	US-10-105-057-2	Sequence 2, Appli
25	1417.5	84.1	316	14	US-10-272-411-19	Sequence 19, Appl
26	1417.5	84.1	316	14	US-10-272-328A-19	Sequence 19, Appl
27	1417.5	84.1	316	14	US-10-326-052-2	Sequence 2, Appli
28	1417.5	84.1	316	14	US-10-167-182-1	Sequence 1, Appli
29	1417.5	84.1	316	14	US-10-460-623-1	Sequence 1, Appli
30	1417.5	84.1	316	16	US-10-664-801-4	Sequence 4, Appli
31	1417.5	84.1	316	16	US-10-664-801-6	Sequence 6, Appli
32	1326.5	78.7	294	9	US-09-871-856-11	Sequence 11, Appl
33	1326.5	78.7	294	9	US-09-865-363-11	Sequence 11, Appl
34	1326.5	78.7	294	9	US-09-871-291-11	Sequence 11, Appl
35	1326.5	78.7	294	9	US-09-877-650-11	Sequence 11, Appl
36	1326.5	78.7	294	14	US-10-405-878-11	Sequence 11, Appl
37	1325	78.6	250	14	US-10-338-785A-1	Sequence 1, Appli
38	1325	78.6	250	16	US-10-611-363-1	Sequence 1, Appli
39	1319	78.3	249	14	US-10-050-902-221	Sequence 221, App
40	1319	78.3	249	14	US-10-050-898-221	Sequence 221, App
41	1319	78.3	249	15	US-10-289-456-82	Sequence 82, Appl
42	1301	77.2	246	14	US-10-167-182-17	Sequence 17, Appl
43	1301	77.2	246	14	US-10-460-623-17	Sequence 17, Appl
44	1293	76.7	245	10	US-09-873-829-2	Sequence 2, Appli
45	1293	76.7	245	13	US-10-017-910-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-813-329-7
; Sequence 7, Application US/09813329
; Patent No. US20020012968A1

```
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor
Class Molecule ("DmTNF") and
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7
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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
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Db    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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RESULT 2

US-09-871-856-13

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; Sequence 13, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
;           Galibert, Laurent
;           Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
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Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        |||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 3

US-09-957-944-6

; Sequence 6, Application US/09957944

; Publication No. US20020086312A1

; GENERAL INFORMATION:

; APPLICANT: Dougall, William C.

; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVATOR OF

; TITLE OF INVENTION: NF-kappa B

; FILE REFERENCE: 3109-A

; CURRENT APPLICATION NUMBER: US/09/957,944

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/235,157

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 317

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-957-944-6

Query Match 100.0%; Score 1685; DB 9; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
        |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
Qy      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        |||
Db      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

```


Qy 301 PDQDATYFGAFKVRDID 317
| | | | | | | | | | | | | | | |
Db 301 PDQDATYFGAFKVRDID 317

RESULT 4

US-09-865-363-13

; Sequence 13, Application US/09865363

; Publication No. US20020086826A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,363

; FILING DATE: 25-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-865-363-13

Query Match 100.0%; Score 1685; DB 9; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 |||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180
 |||
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180

QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
 |||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

QY 301 PDQDATYFGAFKVRDID 317
 |||
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

US-09-871-291-13

; Sequence 13, Application US/09871291

; Publication No. US20020086827A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

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; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGGFFKLSRGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGGFFKLSRGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

```

RESULT 6

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. US20020169117A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

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```

Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180
|
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAHLTINATDIPSGSH 180
|
Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240
|

```

```

Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
          |||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 7

US-10-151-071-10

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; Sequence 10, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-10

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Query Match      100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317

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Db 301 PDQDATYFGAFKVRDID 317

RESULT 8
US-10-218-547-22
; Sequence 22, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relating To
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 317
; TYPE: PRT
; ORGANISM: human
US-10-218-547-22

Query Match 100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
|
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
|
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAH LTINATDIPSGSH 180
|
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAH LTINATDIPSGSH 180

Qy 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
|
Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
|
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
|
Db 301 PDQDATYFGAFKVRDID 317

RESULT 9

US-10-405-878-13

; Sequence 13, Application US/10405878

; Publication No. US20030175840A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/405,878

; FILING DATE: 01-Apr-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-405-878-13

Query Match 100.0%; Score 1685; DB 14; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
 |||

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 |||

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
 |||

Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
 |||

Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300
 |||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 10

US-10-167-182-11

; Sequence 11, Application US/10167182
 ; Publication No. US20030176647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamaguchi, Kyoji
 ; APPLICANT: Yasuda, Hisataka
 ; APPLICANT: Nakagawa, No. US20030176647Aluaki
 ; APPLICANT: Shima, No. US20030176647Aluyuki
 ; APPLICANT: Kinosaki, Masahiko
 ; APPLICANT: Tsuda, Eisuke
 ; APPLICANT: Goto, Masaaki
 ; APPLICANT: Yano, Kazuki
 ; APPLICANT: Tomoyasu, Akihiro
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Washida, Naohiro
 ; APPLICANT: Takahashi, Ken
 ; APPLICANT: Morinaga, Tomonori
 ; APPLICANT: Higashio, Kanji
 ; TITLE OF INVENTION: Antibodies to OCIF-binding Molecules
 ; FILE REFERENCE: FJN-070DV
 ; CURRENT APPLICATION NUMBER: US/10/167,182
 ; CURRENT FILING DATE: 2002-06-11
 ; PRIOR APPLICATION NUMBER: US 09/202,455
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: JP 97808/1997
 ; PRIOR FILING DATE: 1997-04-15
 ; PRIOR APPLICATION NUMBER: JP 151434/1997
 ; PRIOR FILING DATE: 1997-06-09
 ; PRIOR APPLICATION NUMBER: JP 217897/1997
 ; PRIOR FILING DATE: 1997-08-12
 ; PRIOR APPLICATION NUMBER: JP 224803/1997
 ; PRIOR FILING DATE: 1997-08-21
 ; PRIOR APPLICATION NUMBER: JP 332241/1997


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; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: human
US-10-310-793-28

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Query Match          100.0%;   Score 1685;   DB 14;   Length 317;
Best Local Similarity 100.0%;   Pred. No. 2.5e-149;
Matches 317;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12
 US-10-460-623-11
 ; Sequence 11, Application US/10460623
 ; Publication No. US20030208045A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamaguchi, Kyoji
 ; APPLICANT: Yasuda, Hisataka
 ; APPLICANT: Nakagawa, No. US20030208045Aluaki
 ; APPLICANT: Shima, No. US20030208045Aluyuki
 ; APPLICANT: Kinosaki, Masahiko
 ; APPLICANT: Tsuda, Eisuke
 ; APPLICANT: Goto, Masaaki
 ; APPLICANT: Yano, Kazuki
 ; APPLICANT: Tomoyasu, Akihiro
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Washida, Naohiro
 ; APPLICANT: Takahashi, Ken
 ; APPLICANT: Morinaga, Tomonori
 ; APPLICANT: Higashio, Kanji
 ; TITLE OF INVENTION: No. US20030208045A1el Protein and Method for Producing
 the Protein
 ; FILE REFERENCE: FJN-070
 ; CURRENT APPLICATION NUMBER: US/10/460,623
 ; CURRENT FILING DATE: 2003-06-13
 ; PRIOR APPLICATION NUMBER: JP 97808/1997
 ; PRIOR FILING DATE: 1997-04-15
 ; PRIOR APPLICATION NUMBER: JP 151434/1997
 ; PRIOR FILING DATE: 1997-06-09
 ; PRIOR APPLICATION NUMBER: JP 217897/1997
 ; PRIOR FILING DATE: 1997-08-12
 ; PRIOR APPLICATION NUMBER: JP 224803/1997
 ; PRIOR FILING DATE: 1997-08-21
 ; PRIOR APPLICATION NUMBER: JP 332241/1997
 ; PRIOR FILING DATE: 1997-12-02
 ; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-460-623-11

Query Match 100.0%; Score 1685; DB 14; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.5e-149;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH	180

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Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
QY      181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Db      181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSG NSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSG NSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 13

US-10-289-456-79

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; Sequence 79, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-456-79

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Query Match          100.0%; Score 1685; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEG PLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEG PLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
QY      61 VCSVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRR IK 120
Db      61 VCSVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRR IK 120
QY      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180

```

```

Db      121  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 180
Qy      181  KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
Qy      301  PDQDATYFGAFKVRDID 317
         ||||||||||||||
Db      301  PDQDATYFGAFKVRDID 317

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RESULT 14

US-10-202-062-22

; Sequence 22, Application US/10202062

; Publication No. US20040038349A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.,

; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members

; FILE REFERENCE: PF559

; CURRENT APPLICATION NUMBER: US/10/202,062

; CURRENT FILING DATE: 2002-07-25

; PRIOR APPLICATION NUMBER: 60/307,838

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-202-062-22

Query Match 100.0%; Score 1685; DB 15; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121  QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
Qy      181  KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

```

```

Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
          |||||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 15

US-10-664-801-2

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; Sequence 2, Application US/10664801
; Publication No. US20040115199A1
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/10/664,801
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/396,937
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-801-2

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Query Match          100.0%; Score 1685; DB 16; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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QY      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||||
Db      121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

QY      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
          |||||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEEISIEVSNPSLLD 300
          |||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEEISIEVSNPSLLD 300

QY      301 PDQDATYFGAFKVRDID 317
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Db

301 PDQDATYFGAFKVRDID 317

Search completed: November 8, 2004, 18:44:23

Job time : 173 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:23:14 ; Search time 192 Seconds
(without alignments)
949.968 Million cell updates/sec

Title: US-09-787-126-2
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1685	100.0	317	1	TN11_HUMAN	O14788 h tumor nec
2	1417.5	84.1	316	1	TN11_MOUSE	O35235 m tumor nec
3	1396.5	82.9	318	1	TN11_RAT	Q9ese2 r tumor nec
4	1292	76.7	244	2	BAB79693	Bab79693 homo sapi
5	266	15.8	317	2	Q7ZYX9	Q7zyx9 brachydanio
6	265	15.7	304	2	Q7T1F2	Q7t1f2 gallus gall
7	251.5	14.9	281	1	TN10_HUMAN	P50591 homo sapien
8	251.5	14.9	281	2	CAG33176	Cag33176 homo sapi
9	249.5	14.8	299	2	Q6DHG9	Q6dhg9 brachydanio
10	248	14.7	291	1	TN10_MOUSE	P50592 mus musculu
11	240.5	14.3	214	2	Q9DDZ5	Q9ddz5 brachydanio
12	216.5	12.8	287	2	Q90WT9	Q90wt9 gallus gall
13	215.5	12.8	287	2	Q8K3G0	Q8k3g0 rattus norv
14	200	11.9	282	1	TNF6_PIG	Q9bea8 sus scrofa
15	194.5	11.5	280	2	Q861W5	Q861w5 felis silve

16	189	11.2	281	1	TNF6_HUMAN	P48023 homo sapien
17	189	11.2	281	2	AAO43991	Aao43991 homo sapi
18	187.5	11.1	279	2	Q7TMV9	Q7tmv9 mus musculu
19	186	11.0	280	1	TNF6_MACMU	Q9myl6 macaca mula
20	184.5	10.9	252	2	Q8K3Y8	Q8k3y8 mus musculu
21	184.5	10.9	279	1	TNF6_MOUSE	P41047 mus musculu
22	184.5	10.9	279	2	BAC30520	Bac30520 mus muscu
23	182.5	10.8	280	1	TNF6_CERTO	Q9bdn1 cercocebus
24	181	10.7	95	2	Q6UWL7	Q6uwl7 homo sapien
25	181	10.7	95	2	Q6UY13	Q6uy13 homo sapien
26	181	10.7	95	2	AAQ88490	Aaq88490 homo sapi
27	181	10.7	95	2	AAQ89101	Aaq89101 homo sapi
28	179.5	10.7	252	2	Q80YZ0	Q80yz0 mus musculu
29	177.5	10.5	252	2	Q8K3Y7	Q8k3y7 rattus norv
30	176.5	10.5	261	1	TNF5_BOVIN	P51749 bos taurus
31	175.5	10.4	278	1	TNF6_RAT	P36940 rattus norv
32	169.5	10.1	261	1	TNF5_CALJA	Q9bdn3 callithrix
33	167.5	9.9	261	1	TNF5_AOTTR	Q9bdm3 aotus trivi
34	158.5	9.4	261	1	TNF5_HUMAN	P29965 homo sapien
35	158.5	9.4	261	2	AAH71754	Aah71754 homo sapi
36	156.5	9.3	251	2	Q8NFE9	Q8nfe9 homo sapien
37	156.5	9.3	251	2	AAH69435	Aah69435 homo sapi
38	155.5	9.2	261	1	TNF5_MACMU	Q9bdc7 macaca mula
39	155	9.2	272	1	TNF5_CHICK	Q9i8d8 gallus gall
40	152.5	9.1	261	1	TNF5_PIG	Q95mq5 sus scrofa
41	152	9.0	260	1	TNF5_FELCA	O97605 felis silve
42	146	8.7	234	1	TNFA_CAVPO	P51435 cavia porce
43	145.5	8.6	239	1	TN14_MOUSE	Q9qyh9 mus musculu
44	145	8.6	174	1	TN15_HUMAN	O95150 homo sapien
45	145	8.6	260	1	TNF5_CANFA	O97626 canis famil

ALIGNMENTS

RESULT 1

TN11_HUMAN

ID TN11_HUMAN STANDARD; PRT; 317 AA.

AC O14788; O14723; Q96Q17; Q9P2Q3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).

GN Name=TNFSF11; Synonyms=RANKL, TRANCE, OPGL;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Bone marrow, and Peripheral blood;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,

RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,

RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function."
 RL Nature 390:175-179(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lymph node;
 RX MEDLINE=98227661; PubMed=9568710;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation."
 RL Cell 93:165-176(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RT "Determination of human RANKL isoforms."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=97460112; PubMed=9312132;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells."
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation."
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;

```

CC      IsoId=O14788-2; Sequence=VSP_006447;
CC      Name=3;
CC      IsoId=O14788-3; Sequence=VSP_006446;
CC      -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC          spleen, peripheral blood Leukocytes, bone marrow, heart, placenta,
CC          skeletal muscle, stomach and thyroid.
CC      -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC      -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC          by proteolytic processing (By similarity). The cleavage may be
CC          catalyzed by ADAM17.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019047; AAB86811.1; -.
DR      EMBL; AF053712; AAC39731.1; -.
DR      EMBL; AB064269; BAB79694.1; -.
DR      EMBL; AB061227; BAB71768.1; -.
DR      EMBL; AB064270; BAB79695.1; -.
DR      EMBL; AF013171; AAC51762.1; -.
DR      EMBL; AB037599; BAA90488.1; -.
DR      HSSP; O35235; 1JTZ.
DR      Genew; HGNC:11926; TNFSF11.
DR      MIM; 602642; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      GO; GO:0030316; P:osteoclast differentiation; NAS.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Alternative splicing; Cytokine; Differentiation; Glycoprotein;
KW      Receptor; Signal-anchor; Transmembrane.
FT      CHAIN      1      317      Tumor necrosis factor ligand superfamily
FT                                     member 11, membrane form.
FT      CHAIN      140     317      Tumor necrosis factor ligand superfamily
FT                                     member 11, soluble form (By similarity).
FT      DOMAIN      1      47      Cytoplasmic (Potential).
FT      TRANSMEM     48      68      Signal-anchor for type II membrane
FT                                     protein (Potential).
FT      DOMAIN      69     317      Extracellular (Potential).
FT      SITE       139     140      Cleavage (By similarity).
FT      CARBOHYD    171     171      N-linked (GlcNAc . . .) (Potential).
FT      CARBOHYD    198     198      N-linked (GlcNAc . . .) (Potential).
FT      VARSPLIC     1      47      Missing (in isoform 3).

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FT /FTid=VSP_006446.
 FT VARSPLIC 1 73 Missing (in isoform 2).
 FT /FTid=VSP_006447.
 FT CONFLICT 194 194 A -> G (in Ref. 4).
 SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.2e-134;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

 QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

 QY 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

 QY 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH FYSINVG GFFKLRS GEEISIEVSNPSLLD 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH FYSINVG GFFKLRS GEEISIEVSNPSLLD 300

 QY 301 PDQDATYFGAFKVRDID 317
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 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

TN11_MOUSE

ID TN11_MOUSE STANDARD; PRT; 316 AA.
 AC O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 DE (OCIF).
 GN Name=Tnfsf11; Synonyms=RANKL, Trance, OPGL;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma;
 RX MEDLINE=97460112; PubMed=9312132;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,

RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=98032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow;
 RX MEDLINE=98227661; PubMed=9568710;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
 RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma;
 RX MEDLINE=98188248; PubMed=9520411;
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.

RX MEDLINE=99240759; PubMed=10224132;
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family
 RT member involved in osteoclastogenesis and dendritic cell survival.";
 RL J. Biol. Chem. 274:13613-13618(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
 CC but not in nonlymphoid tissues and is abundantly expressed in T
 CC cells but not in B cells. A high level expression is also seen in
 CC the trabecular bone and lung.
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
 CC alveolar mammary structures during pregnancy, resulting in death
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
 CC profound growth retardation at several skeletal sites, including
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,
 CC with thick, irregular growth plates and a relative increase in
 CC hypertrophic chondrocytes.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR EMBL; AB032771; BAA97257.1; -.
DR EMBL; AB032772; BAA97258.1; -.
DR EMBL; AB036798; BAA97259.1; -.
DR PDB; 1IQA; X-ray; A/B/C=157-316.
DR PDB; 1JTZ; X-ray; X/Y/Z=146-316.
DR MGD; MGI:1100089; Tnfsf11.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042804; F:protein homooligomerization activity; IDA.
DR GO; GO:0045453; P:bone resorption; IDA.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0001503; P:ossification; IMP.
DR GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW 3D-structure; Alternative splicing; Cytokine; Differentiation;
KW Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
KW Transmembrane.
FT CHAIN 1 316 Tumor necrosis factor ligand superfamily
FT member 11, membrane form.
FT CHAIN 139 316 Tumor necrosis factor ligand superfamily
FT member 11, soluble form.
FT DOMAIN 1 48 Cytoplasmic (Potential).
FT TRANSMEM 49 69 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 70 316 Extracellular (Potential).
FT SITE 138 139 Cleavage.
FT CARBOHYD 197 197 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 262 262 N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC 1 117 Missing (in isoform 3).
FT /FTId=VSP_006448.
FT VARSPLIC 14 44 SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
FT isoform 2).
FT /FTId=VSP_006449.
FT CONFLICT 99 99 G -> D (in Ref. 2).

```

FT	CONFLICT	141	143	Missing (in Ref. 5).
FT	STRAND	164	169	
FT	TURN	171	172	
FT	STRAND	181	182	
FT	STRAND	186	187	
FT	TURN	191	192	
FT	STRAND	194	196	
FT	STRAND	198	201	
FT	TURN	202	203	

Query Match 84.1%; Score 1417.5; DB 1; Length 316;
 Best Local Similarity 84.3%; Pred. No. 6.1e-112;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ	59
		:	
Db	1	MRRASRDYGKYLRSEEMGGGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
		: : : : :	
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM	118
Qy	120	KQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGS	179
		: :	
Db	119	KQAFQGA VQKELQHIVGPQRFSGAPAMMEG SWLDVAQRGKPEAQPF AHLTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
		: : :	
Db	179	HKVTLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH FYSINVGGFFKLRSGEEISIEVSNP SLL	299
		: :	
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNW SGNSEFH FYSINVGGFFKLRAGEEISIQVSNP SLL	298
Qy	300	DPDQDATYFGAFKVRDID	317
Db	299	DPDQDATYFGAFKVQDID	316

RESULT 3
 TN11_RAT
 ID TN11_RAT STANDARD; PRT; 318 AA.
 AC Q9ESE2; Q91ZI9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF).
 GN Name=Tnfsf11; Synonyms=RANKL, Trance, Opgl;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Tibial bone;
 RX MEDLINE=20540945; PubMed=11092398;
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
 RA Zheng M.H.;
 RT "Cloning, sequence and functional characterization of the rat
 RT homologue of receptor activator of NF-kB ligand.";
 RL J. Bone Miner. Res. 15:2178-2186(2000).
 RN [2]
 RP SEQUENCE OF 266-318 FROM N.A.
 RC STRAIN=Fischer 344;
 RX MEDLINE=21662371; PubMed=11804028;
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
 RA Marks S.C. Jr.;
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
 RL Int. J. Dev. Biol. 45:853-859(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 DR EMBL; AF187319; AAG17031.1; -.
 DR EMBL; AF425669; AAL23963.1; -.
 DR HSSP; O35235; 1JTZ.
 DR RGD; 620784; Tnfsf11.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
 KW Transmembrane.
 FT CHAIN 1 318 Tumor necrosis factor ligand superfamily
 FT member 11, membrane form.

FT	CHAIN	141	318	Tumor necrosis factor ligand superfamily
FT				member 11, soluble form.
FT	DOMAIN	1	47	Cytoplasmic (Potential).
FT	TRANSMEM	48	68	Signal-anchor for type II membrane
FT				protein (Potential).
FT	DOMAIN	69	318	Extracellular (Potential).
FT	SITE	140	141	Cleavage (By similarity).
FT	CARBOHYD	199	199	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	264	264	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	317	317	I -> M (in Ref. 2).
SO	SEQUENCE	318 AA;	35370 MW;	4B87A4D706AD098F CRC64;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ	59
Db	1	MRRANRDYGYKYLRGSEEMGSCPGVPHEGPLHPAPSAPAPAPPPAASRFMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
Db	61	VVCSIALFLYFRAQMDPNRISEDSTRCFYRILRLRENTGLQDSTLESEDEALPDSCRRM	120
Qy	120	KQAFQGA VQKELQHIVGSGHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGS	179
Db	121	KQAFQGA VQRELQHIVGPQRFSGVPAMMEGSWLDVARRGKPEAQPF AHLTINAADIPSGS	180
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
Db	181	HKVSLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSV PADYLQLM	240
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLL	299
Db	241	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG GFFKL RAGEEISVQVSNPSLL	300
Qy	300	DPDQDATYFGAFKVRDID	317
Db	301	DPDQDATYFGAFKVQDID	318

RA Tatsumi M., Uematsu H., Hirokawa K.;
 RT "Regulation of osteoclastogenesis by three human RANKL isoforms
 RT expressed in NIH3T3 cells.";
 RL Biochem. Biophys. Res. Commun. 314:1021-1027(2004).
 DR EMBL; AB064268; BAB79693.1; -.
 KW Receptor.
 SQ SEQUENCE 244 AA; 27690 MW; C827590684B6B83C CRC64;

Query Match 76.7%; Score 1292; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 2e-101;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGA VQKELQH 133
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGA VQKELQH 60

 QY 134 IVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSHK VSLSSWYH DRGW 193
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 IVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSHK VSLSSWYH DRGW 120

 QY 194 AKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSH 253
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 AKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSH 180

 QY 254 TLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQDATYFGAFKV 313
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 TLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQDATYFGAFKV 240

 QY 314 RDID 317
 ||||
 Db 241 RDID 244

RESULT 5

Q7ZYX9

ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.
 AC Q7ZYX9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tnfsf101 protein.
 GN Name=tnfsf101;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC044336; AAH44336.1; -.
 DR HSSP; P50591; 1D2Q.
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 15.8%; Score 266; DB 2; Length 317;
 Best Local Similarity 26.6%; Pred. No. 4.1e-14;
 Matches 79; Conservative 66; Mismatches 122; Indels 30; Gaps 9;

Qy 42 PAASR-----SMFVALLGLGLG--QVVCSSVALFFYFRAQMDPNRISEDGTHCIYRILRL 93
 || || ::||: : : | : : || | | : : | || |
 Db 24 PANSRGRDSPSKLWIAMVVVVVVLQIASTTGLFVYL--NMSLSQVKSQGVTEELRCLGL 81

 Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDGSWLD 153
 | :| : :| :| : : : :| :| :| :
 Db 82 -LNLVGLKDQDIPEDLAQLFGEPCMKLAEGIKAYISKVTDISIISKQTLHAARTRTHSYNTT 140

 Qy 154 LAK-RSKLEAQPFHAHTINATDIPS-----GSHKVSLSWYHDRGWAKISN 198
 :| : : :| ||| : : | : : :| : :| :| :
 Db 141 GSKFMTTVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLN 200

 Qy 199 MTFNSNGKLIVNQDGFYYLYANICFRHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLM 256
 || :||:| | ||| ||| : ||: | : : ||| | :
 Db 201 MTLTNGRLRVPQDGRYYLYSQVYFRYPSPSDSQSSVSHQLVQCIYKKTSYLNPIQ--LL 258

 Qy 257 KGGSTKYWSGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
 || || | : :|| : :| || :||:| : : ||:| : : : :||| : :
 Db 259 KGVGTKCWAPDAEYALHSVYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 315

Q7T1F2

Query Match 15.7%; Score 265; DB 2; Length 304;
Best Local Similarity 27.3%; Pred. No. 4.7e-14;
Matches 82; Conservative 56; Mismatches 126; Indels 36; Gaps 12;

Qy	38	PHQPPAASRSMFVALLGLGLQVVCVALFFYFRAQMDP--NRISEDGTHCI--YRILRL	93
Db	3	PAGGPSPAHTCGAVLVAVLLQSVCAVITYIYFTNELKQLWDTYRSRGTA CLTGEELGDL	62
Qy	94	HENADFQD TTLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLD	153
Db	63	IQNL D---VVESKDR--VADPCWQVKWHLGKLIKMM SRI-----LQENMSAINGDR TQ	111
Qy	154	-LAKRSKLEAQP----FAHLTINATDIPSGSHKV-----SLSSWYHD-RGWAKISNM	199
Db	112	ALSRRDEPPQGPTLRIA AHLTGSSKRSSASPHNYLSYRGIGHKIH SWESSRRGHSFLYNV	171
Qy	200	TFSNGKLIVNQDGFYYLYANICFRHHET----SG--DLATEYLQLMVYVTKTSIKIPSSH	253
Db	172	ELWNGELVVPQTGFYYIYSQTYFRFRENED EDSGLLERIKNPKQLVQYIYKLT-NYPDPI	230
Qy	254	TLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQDATYFGAFKV	313
Db	231	LLMKSARTSCWSKKA EYGLYSVYQGGV FQLKREDRIFVSVSNSDIVDMDKEASFFGAFMI	290

RESULT 7

TN10_HUMAN

ID TN10_HUMAN STANDARD; PRT; 281 AA.

AC P50591;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).

GN Name=TNFSF10; Synonyms=TRAIL, APO2L;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96111955; PubMed=8777713;

RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,

RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

RA Goodwin R.G.;

RT "Identification and characterization of a new member of the TNF family
RT that induces apoptosis.";

RL Immunity 3:673-682(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=96278649; PubMed=8663110;

RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,

RA Ashkenazi A.;

RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";

RL J. Biol. Chem. 271:12687-12690(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE=20017054; PubMed=10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5."
 RL Mol. Cell 4:563-571(1999).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed=10542098; DOI=10.1038/14935;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation."
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE=99413670; PubMed=10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity."
 RL Immunity 11:253-261(1999).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung
 CC and prostate.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U37518; AAC50332.1; -.
 DR EMBL; U57059; AAB01233.1; -.
 DR EMBL; BC032722; AAH32722.1; -.
 DR PDB; 1D0G; X-ray; A/B/D=114-281.
 DR PDB; 1D2Q; X-ray; A=114-281.
 DR PDB; 1D4V; X-ray; B=119-281.
 DR PDB; 1DG6; X-ray; A=91-281.
 DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.
 DR Genew; HGNC:11925; TNFSF10.
 DR MIM; 603598; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
KW Transmembrane; Zinc.
FT DOMAIN 1 17 Cytoplasmic (Potential).
FT TRANSMEM 18 38 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 39 281 Extracellular (Potential).
FT METAL 230 230 Zinc.
FT STRAND 123 127
FT STRAND 149 150
FT STRAND 163 165
FT STRAND 167 170
FT TURN 171 172
FT STRAND 173 176
FT STRAND 180 193
FT TURN 198 199
FT STRAND 205 213
FT STRAND 220 228
FT TURN 233 234
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT HELIX 263 265
FT STRAND 266 267
FT TURN 270 272
FT STRAND 274 279
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 14.9%; Score 251.5; DB 1; Length 281;
Best Local Similarity 24.1%; Pred. No. 5.9e-13;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy 42 PAASRSMFVALLGLGLGQVVCVVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
|: :: : :: | | : | : || :: :: | : | | | :
Db 10 PSLGQTCVLIVIFTVLLQSLCAVAVTYVYFTNELKQMDKYSGIACF-----LKED---- 61
Qy 100 QDTTLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDGWSWLDLAKRSK 159
|: : | : : | : | : | : | : | : : : : : : :
Db 62 -DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILRTSEETI-----STVQEKQ 107
Qy 160 LEAQPF-----AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
| | : | | | : : : | : | | : : | :
Db 108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNL 167


```

Qy      200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
          ||::: ||::: || | : ||::: | : | ||
Db      168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy      260 STKYWSGNSEFHFYSINVGGFKLRSGEIEISIEVSNPSSLDPDQDATYFGAFKV 313
          ||::: ||::: ||::: | : | : | : | : | : | : | : |
Db      227 RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

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CAG33176

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ID      CAG33176      PRELIMINARY;      PRT;      281 AA.
AC      CAG33176;
DT      01-JUN-2004 (TrEMBLrel. 27, Created)
DT      01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT      01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE      TNFSF10 protein.
GN      TNFSF10.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT      "Cloning of human full open reading frames in Gateway(TM) system entry
RT      vector (pDONR201).";
RL      Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; CR456895; CAG33176.1; -.
SQ      SEQUENCE      281 AA;  32509 MW;  DDAAAF78DAAB2F6D CRC64;

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Query Match 14.9%; Score 251.5; DB 2; Length 281;
Best Local Similarity 24.1%; Pred. No. 5.9e-13;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy	42	PAASRSMFVALLGLGLGQVVCVSVALFFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF	99
		: :: : :: : : :: :: :	
Db	10	PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMMDKYSKSGIACF-----LKED---	61
Qy	100	QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK	159
		: : : : :: : :: : : : : : : : : : : : :	
Db	62	-DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILRTSEETI-----STVQEKQ	107
Qy	160	LEAQPF-----AHLT-----INATDIPSGSHKVSL-----SSWYHDR-GWAKISNM	199
Db	108	QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL	167
Qy	200	TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVVYTKTSIKIPSSHTLMKGG	259
		: : : : : : : : : : :	
Db	168	HLRNDELVIHEKGFFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA	226
Qy	260	STKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV	313
		:: : : : : : : : :::	
Db	227	RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV	280

RESULT 9

Q6DHG9

ID Q6DHG9 PRELIMINARY; PRT; 299 AA.
 AC Q6DHG9;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC076005; AAH76005.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 14.8%; Score 249.5; DB 2; Length 299;
 Best Local Similarity 28.1%; Pred. No. 9.5e-13;
 Matches 85; Conservative 49; Mismatches 126; Indels 43; Gaps 13;

Qy 44 ASRSM-FVALLGLG--LGQVVCVALFFYFRAQMDPNR--ISEDGTHCIYRI-LRLHENA 97
 :| :| :: || | | : | || : : |: | || :
 Db 6 SSHTMQYIGLLLLLAAILLQTIHAVVTFIYFSNVLSTMKETFSKSSVSCIMRANLRTIKQ 65
 Qy 98 DFQDTTLESQDTKLIPDSCRRIKQ-----AFQGA VQKELQHIVGSQHRAEKAMVDG 149
 : | :| | | :: | : ||| : | : | ::|
 Db 66 ELNGA--EGKD----DPCWQVTQQLHFLIEKSMSSRYQKEITSAVKDEVSRVLP SLVIQ 118

Qy 150 SWLDLAKRSKLEAQPFHAHLTINATDIPSG--SHKV---SLSSWYHDRGWAKISNMTFSNG 204
 | : | | : | | : : | : | | : | | : | : | : |
 Db 119 DQED-SSRPKIAAHVTGSGYTPSEKDGAGLPNRKVYQKIQSWESEKGLAFLQNLSDG 177

Qy 205 KLIVNQDGFYYLYANICFRH---HETSGDLATEY-----LQLMVYVTKTSIKIP 250
 : | : | | | : | : | | | | | | : | | : | : |
 Db 178 ELVVPQAGLYIYSQTYFRHTLIEEDESAREDEYSGMGESVRGKPMQLQYVYKKVSSYQVP 237

Qy 251 SSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEESIEVSNPSSLDPDQDATYFGA 310
 | | | | | | : | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
 Db 238 I--LLMKNARTTCWSRDSEYGLYSIQAGLFQLGSGDRVFVTVSNVSTIDMDEKSSFFGA 295

Qy 311 FKV 313
 | |
 Db 296 FLV 298

RESULT 10

TN10_MOUSE

ID TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN Name=Tnfsf10; Synonyms=Trail;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF family
 RT that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Widespread.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE TRAIL-like protein.
 GN Name=tnfsf101;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J., Goetz F.W.;
 RT "Molecular cloning and expression of a TNF receptor and two TNF
 RT ligands in the fish ovary."
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
 DR EMBL; AF250041; AAG47640.1; -.
 DR HSSP; P50591; 1D2Q.
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 14.3%; Score 240.5; DB 2; Length 214;
 Best Local Similarity 28.6%; Pred. No. 3.5e-12;
 Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;

Qy 118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAK-RSKLEAQPF AHLTINATDIP 176
 :: : : : | | : | : | : : | : : : | | | : :
 Db 2 KLAEGIKAYISKV TDSIISKQTLHAARTQTHSYNTTGSKFMTTVMQRPSAHLTLSSASDN 61

 Qy 177 S-----GSHKVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICF 222
 | : : : | : | : | | : | | | | | : : |
 Db 62 SRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLNMTLTNGRLRVPQDGRYYLYSQVYF 121

 Qy 223 RHHETS-GDLATEY LQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280
 | : | | : : || : : || | : || | | : : : : : : ||
 Db 122 RYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQ--LLKGVGTCWAPDAEYALHSVYQGGL 179

 Qy 281 FKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
 | : | : | : : | : | : : : : : : : : : : : : : :
 Db 180 FELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212

RESULT 12

Q90WT9

ID Q90WT9 PRELIMINARY; PRT; 287 AA.

AC Q90WT9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE TNF-related apoptosis inducing ligand-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR HSSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 12.8%; Score 216.5; DB 2; Length 287;
Best Local Similarity 24.7%; Pred. No. 5.7e-10;
Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;

Qy 80 SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRKQAFQGAVQKELQHIVGSQH 139
| : | : | : | : : : : : | | : : : | : : :
Db 51 SSEELRCLQLINQQEGSNLEEL-----ISNQSLKLANTIKAYVATVTENVISRSV 102
Qy 140 I-RAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIP-----SGSHKVSLSW 187
: | : | : | : | : | : | : | : | : | : | : : : |
Db 103 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW 160
Qy 188 YHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQLMVYVT-KTS 246
: : | : | : : | : | : | : | : | : | : | : : : | : | :
Db 161 EDSTIHSHLQNITYRDGRLRVNQAGKYYVYSQIYFRYSRDGAGARVSVPLVQCINWKTS 220
Qy 247 IKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDAT 306
| : | : | : | : : : : | : | : : | : : : | : : : | : :
Db 221 YSQPI--LLLKGVGTKCWAPEAEYGLHALYQGGLFELKAGDELFSVSSLAIDYSDAAS 278
Qy 307 YFGAFKV 313
| | | | : :
Db 279 YFGAFRL 285

RESULT 13

Q8K3G0

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.
AC Q8K3G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

ID TNF6_PIG STANDARD; PRT; 282 AA.
 AC Q9BEA8; Q95M04; Q95N10;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN Name=TNFSF6; Synonyms=FASL;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21322533; PubMed=11429161; DOI=10.1089/107999001300177493;
 RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
 RT "Molecular cloning, characterization, and expression of porcine Fas
 RT ligand (CD95 ligand).";
 RL J. Interferon Cytokine Res. 21:305-312(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Guanxi bama miniature pig;
 RA Zhu N., Young Y.;
 RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RA Tsuyuki S., Kono M., Bloom E.T.;
 RT "Cloning and potential utility of porcine Fas ligand: overexpression
 RT in porcine cells protects them from attack by human cytolytic cells.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
 RX MEDLINE=21653191; PubMed=11792426;
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
 RT with human gene.";
 RL Mol. Immunol. 38:581-586(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- INDUCTION: By IL-18.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; AB027297; BAB40919.1; -.
 DR EMBL; AY033634; AAK56449.1; -.
 DR EMBL; AF397407; AAK84408.1; -.
 DR EMBL; AB069764; BAB64291.1; -.
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01681; FASLIGAND.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
 FT CHAIN 1 282 Tumor necrosis factor ligand superfamily
 FT member 6, membrane form.
 FT CHAIN 131 282 Tumor necrosis factor ligand superfamily
 FT member 6, soluble form (By similarity).
 FT DOMAIN 1 82 Cytoplasmic (Potential).
 FT TRANSMEM 83 103 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 104 282 Extracellular (Potential).
 FT DOMAIN 4 70 Pro-rich.
 FT DOMAIN 45 56 Poly-Pro.
 FT SITE 130 131 Cleavage (By similarity).
 FT DISULFID 203 234 Potential.
 FT CARBOHYD 185 185 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 251 251 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 261 261 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 5 5 F -> L (in Ref. 4).
 FT CONFLICT 57 57 T -> P (in Ref. 2).
 SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;

Query Match 11.9%; Score 200; DB 1; Length 282;
 Best Local Similarity 23.0%; Pred. No. 1.4e-08;
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

Qy 22 PGAPHEGPLHAPPPAPHPQPPAA---SRSM-----FVA 51
 || | | ||| | || || : ||
 Db 37 PGRP--GQRRPPPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMFFMVLVA 94
 Qy 52 LLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL 111
 |:||||| :| | : :| |:| :|
 Db 95 LVGLGLG-----MFQLFHLQKE-----LTELRRESASQRHT----- 124
 Qy 112 IPDSCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFHAHLT-- 169
 : |: :| :: :|| | : |||

```

Db      125 -----ESSLEKQIGHPNLPSEKK-----ELRKVAHLTGK 153
QY      170 INATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSG 229
      | : || | | : | : : | | : | | | : | : | : | :
Db      154 PNSRSIP-----LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCN- 204
QY      230 DLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGFFKL 283
      : | || | : | | | : | | | : | : | : | : | :
Db      205 ---NQPLSHKVY-TRNS-RYPQDLVMEGKMMNYCTTGQMWARSS-----YLGAVFNL 252
QY      284 RSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
      | : : : || || : : : | : || : | :
Db      253 TSADHLYVNVSELSLVNFEESKTFGLYKL 282

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RESULT 15

Q861W5

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ID   Q861W5          PRELIMINARY;          PRT;    280 AA.
AC   Q861W5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fas ligand.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99053606; PubMed=9839871;
RA   Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
RA   Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL   Vet. Immunol. Immunopathol. 65:161-172(1998).
DR   EMBL; AB009280; BAC76426.1; -.
DR   HSSP; P01374; 1TNR.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE    280 AA;  31361 MW;  6AA7E2DE1F1A6B5C CRC64;

```

Query Match

11.5%; Score 194.5; DB 2; Length 280;

Best Local Similarity 22.8%; Pred. No. 4.1e-08;
 Matches 74; Conservative 40; Mismatches 98; Indels 113; Gaps 12;

```

Qy      20 GGPG----APHEGPLHAPPPAPHPAASRSM-----FVALLGLG 56
      | ||      | |      |||| | ||      :      |||:||||
Db      38 GRPGQRRPPPPPPPTLPPPPPPPLPPLPLPPLKTRRDHNTGLCLLMFFMVLVALVGLG 97

Qy      57 LGQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSC 116
      ||      :| | |      | | : : : | :
Db      98 LG-----MFQLFHLQ-----KELAELESTSQKH----- 121

Qy     117 RRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLT--INATD 174
      | | : : | : : ||      | : |||| | :
Db     122 -----VASSLEKQIGQLNPPSEKR-----ELRKVAHLTGKPNRSR 156

Qy     175 IPGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATE 234
      ||      | | : | : : | | : | | : : | | : :
Db     157 IP-----LEWEDTYGIALVSGVKYKKGGLVINDTGMVFVYSKVNFRGQSCN----NQ 204

Qy     235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRSCEE 288
      | || : : | | || : | | : : | : : | | | :
Db     205 PLNHKVYMRNS--KYPQDLVLMGKMMNYCTTGQMWARSS-----YLGA VFNLT SADH 255

Qy     289 ISIEVSNPSLLDPDQDATYFGAFKV 313
      : : || || : : | : || : :
Db     256 LYVNVSELSLVSFEEKTFEGLYKL 280

```

Search completed: November 8, 2004, 18:32:13
 Job time : 194 secs